

SEQUENCE LISTING

<110> NOVARTIS AG

C / <120> Improvements in or relating to organic compounds

<130> S-137-1103/SG/A/SGS/PCT /

<140> US 09/180,798

<141> November 16, 1999

<160> 33

<170> PatentIn Ver. 2.1

<210> 1

<211> 6695

<212> DNA

<213> Daucus carota

<220>

<221> misc_feature

<222> (3696)..(6617)

<223> CDS

<220>

<221> intron

<222> (3731)..(3802)

<220>

<221> intron

<222> (3851)..(3979)

<220>

<221> intron

<222> (4124)..(4211)

<220>

<221> intron

<222> (4284)..(4357)

<220>

<221> intron

<222> (4430)..(4528)

<220>

<221> intron

<222> (4642)..(4757)

<220>

<221> intron

<222> (4890)..(4967)

<220>

<221> intron

<222> (5295)..(5803)



[1]

<220>
<221> intron
<222> (6197)..(6339)

```
<220>
<221> misc_feature
<222> (1)..(6695)
<223> n = a, t, c, or g
```

2

gctggcaatt atatcttacg aacttacgag tatacagaac ttgttatatta ggttcagatg 2820
agtggctgta gtagaacacc ttaagcaaga acttaatcat gaggttcaa ccttttaact 2880
ttcttttttag atttttcaa gtttatggaa aattgtacct catgatcgta gtttcttc 2940
ataaaacttc catataagtc cgtttcttga cgttttcatg taagctgtt acgagtgatt 3000
attagcggtt ctttcaataa tcataatgtg tctcaacttg atgaggcctg tacttattat 3060
tgcacccctgc acttaacctt gatcctcatg tcatcttgat tgctcatagtc tactaaccga 3120
gttgaacatg gtttatcatg tctttgagg taacaatgt a gtttcacccct ctgtccttga 3180
tataaggta aggcttgcac ctcccactag ctttcgtt gtttattcac agttcacaca 3240
cctactagca ctgttcacccct ctgttcttt gtccgcaaat agtaagaagt ttcttcgca 3300
taatagtggta tgatcattta agaaatagtg aatcaaattt tcgtgttatt gtgtttgtac 3360
tttggaaatta aatgagttgc tgaacattgt tgctgtttat cggtgtcaag gctttgccaa 3420
ggaaggcgt tagtaagagt gggcatccaa ggcctttat cttgaagggg cgggcggcac 3480
gttggattt ctgggtgtct attagaggac attatctata tatactgatt atttatttata 3540
atataaaatca actactat ttttctttgt aatgtttata tagaaatccc actcgtaaac 3600
ttgacaaata ccattgaaat atttgaacct aattaatttag tagtgtcagg tttaaattca 3660
aactcattta atttacttt aaaaataat tctatatgaa tcgtAACAGT ataaatataat 3720
taaattacat gtatgtgtgc ctatataatgc ctgtatgtct aatagactcc aagacggctg 3780
ctcttactgc ctaggcgtcc aggcaattca ctgtatgtt ctttgacaaa tatggggttc 3840
gtatgacatt gttggggatc cctatactg gattcctgtt ttgcgtaccc tctgttcaat 3900
tgattttcat tgatgttagta ttactagttt tataaattatt ctttattgca ataatttaac 3960
tggagttta caatgacagg gagcttaca gcaataacat aagtggacca attccttagtg 4020
atcttggaa tctgacaaat ttggtagct tggacctata catgaatagc ttctctggac 4080
ctataccgga cacatttagga aagcttacaa ggctaagattt ctgtatgac tacaatctt 4140
caactagttt taacttaatg caatttgattt atccttcaat gttgattgatt atatcacaaa 4200
ttactggata ggcgtctcaa caacaactgc ctctctggc caattccaaat gtcactgact 4260
aatattacaa ctcttcaatg ctgtaaatgtt ttccgacott tccagatagt ttgtttgtt 4320
tggatgtttc aattttaata ctaaatatgt tcatcaggga ttatcaaaac aatcggttat 4380
caggaccagt accggataat ggctcattttt ctttggattt acctatcagg tttatgtca 4440
gtaatatctt taatattatg ttcttactt ctactgaa aactatgata atattttttt 4500
tctccttcat atattatcac ttccgactt ttggacataa ttgtttaat tttgttgc 4560
taacttggag gccctgcctt ggatctcccc cattttctcc accacccctcg ttcatccac 4620
catcaacagt acaggcctcca ggttggattt tttttatattt aattttccgtt attaattttt 4680
tgactgtaaa aatttgggtt aatttccatca gtttgcataa aagtattttt cttctttctc 4740
ttcttattat tatgaaggac aaaatggtc cactggagctt attgttgggg gagtagctgc 4800
tggatgtctt ttactgtttt ctgcacccctgc aatggcattt gcatgggtggc ggagaagaaa 4860
accggcggaaa catttctttt atgttgcagg ttagtccctgt aaatagatat ctattgaagc 4920
gttactgttc tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 4980
agaagtgcac ctttgtcaac tgaaggggtt ttctctgtca gaaatggcaag tgcacccggaa 5040
tacttttagt accatcccttgc aaggggggtt atttggtaag gtgtataagg gacggcttgc 5100
tggatgtctt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 5160
gttactgttc tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 5220
acgttggatcc tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 5280
aagtgttgcg tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 5340
tggatgtctt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 5400
cagatcttta tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 5460
gttactgttc tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 5520
actggatgtctt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 5580
ttcaacttgg tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 5640
attagtcattt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 5700
ttatggccct tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 5760
ttgatgtctt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 5820
tcccccgtt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 5880
attggatgtctt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 5940
attggacaa gaaatgggggtt tttttttttt tttttttttt tttttttttt tttttttttt 6000
caaggatacc catgttacga ctgtgttaag gggatggat tttttttttt tttttttttt 6060
cctctcgact ggaaagtcat cagagaagac cgatgtctt tttttttttt tttttttttt 6120
agagtcattt actggacaga gggtttttga ttttgcgtcc ttttgcgtcc atgtatgtt 6180

tatgttggat gattgggtat gtgtcccggt tgttccttg gttattttt tcacatatta 6240
gtgcctacta ctttgtgtg gccccttgg tttatccct gcctgtattt gattcttagt 6300
catgttatgc atattgacct gctttcaat gtcttttagg taaaaggct tttgaaagag 6360
aaaaagttgg agatgtcggt cgatcctgac ctgcagaaca attacattga cacagaagtt 6420
gagcagctt ttcaagttagc attactctgt acccagggtt cgccaatgga gcggcctaag 6480
atgtcagagg tagtccgaat gcttgaaggt gatggccctt cagaaaagtg ggacgagtgg 6540
caaaaagttg aagtcatcca tcaagacgta gaattagtc cacatcgaac ttctgaatgg 6600
atccttagact cgacagataa cttgcattgtt ttgttattat ctggtccaag ataaaacagca 6660
tataaaatgt aatgaaatata atattttta tggtt 6695

<210> 2
<211> 1815
<212> DNA
<213> Daucus carota

<220>
<221> CDS
<222> (94)..(1752)

<400> 2
gacaaataacc attgaaatat ttgaacctaa ttaatttagta gtgtcagggtt taaattcaaa 60
ctcatttaat tttactttaa aaaataattc tat atg aat cgt aac agt ata aat 114
Met Asn Arg Asn Ser Ile Asn
1 5

ata tta aat tac atg cag ttc act gat gct tac ctt gac aaa tat ggg 162
Ile Leu Asn Tyr Met Gln Phe Thr Asp Ala Tyr Leu Asp Lys Tyr Gly
10 15 20

gtt ctt atg aca ttg gag ctt tac agc aat aac ata agt gga cca att 210
Val Leu Met Thr Leu Glu Leu Tyr Ser Asn Asn Ile Ser Gly Pro Ile
25 30 35

cct agt gat ctt ggg aat ctg aca aat ttg gtg agc ttg gac cta tac 258
Pro Ser Asp Leu Gly Asn Leu Thr Asn Leu Val Ser Leu Asp Leu Tyr
40 45 50 55

atg aat agc ttc tct gga cct ata ccg gac aca tta gga aag ctt aca 306
Met Asn Ser Phe Ser Gly Pro Ile Pro Asp Thr Leu Gly Lys Leu Thr
60 65 70

agg cta aga ttc ttg cgt ctc aac aac agc ctc tct ggt cca att 354
Arg Leu Arg Phe Leu Arg Leu Asn Asn Ser Leu Ser Gly Pro Ile
75 80 85

cca atg tca ctg act aat att aca act ctt caa gtc ctg gat tta tca 402
Pro Met Ser Leu Thr Asn Ile Thr Thr Leu Gln Val Leu Asp Leu Ser
90 95 100

aac aat cgg cta tca gga cca gta ccg gat aat ggc tca ttt tct ttg 450
Asn Asn Arg Leu Ser Gly Pro Val Pro Asp Asn Gly Ser Phe Ser Leu
105 110 115

ttt aca cct atc agt ttt gcc aat aat ttg aat tta tgt gga ccc gta 498
Phe Thr Pro Ile Ser Phe Ala Asn Asn Leu Asn Leu Cys Gly Pro Val

120	125	130	135	
act ggg agg ccc tgc cct gga tct ccc cca ttt tcg cca cca cct ccg				546
Thr Gly Arg Pro Cys Pro Gly Ser Pro Pro Phe Ser Pro Pro Pro Pro				
140		145		150
tcc atc cca cca tca aca gta cag cct cca gga caa aat ggt ccc act				594
Phe Ile Pro Pro Ser Thr Val Gln Pro Pro Gly Gln Asn Gly Pro Thr				
155		160		165
gga gct att gct ggg gga gta gct ggt gct gct tta ctg ttt gct				642
Gly Ala Ile Ala Gly Gly Val Ala Ala Gly Ala Ala Leu Leu Phe Ala				
170		175		180
gca cct gca atg gca ttt gca tgg tgg cgg aga aga aaa ccg cga gaa				690
Ala Pro Ala Met Ala Phe Ala Trp Trp Arg Arg Arg Lys Pro Arg Glu				
185		190		195
cat ttc ttt gat gtg cca gct gaa gag gac cca gaa gtg cac ctt ggt				738
His Phe Phe Asp Val Pro Ala Glu Glu Asp Pro Glu Val His Leu Gly				
200		205		210
caa ctg aag agg ttt tct ctg cga gaa ttg caa gtc gca acg gat act				786
Gln Leu Lys Arg Phe Ser Leu Arg Glu Leu Gln Val Ala Thr Asp Thr				
220		225		230
ttt agt acc ata ctt gga aga ggt gga ttt ggt aag gtg tat aag gga				834
Phe Ser Thr Ile Leu Gly Arg Gly Phe Gly Lys Val Tyr Lys Gly				
235		240		245
cgc ctt gct gat ggc tca ctt gta gca gtt aaa agg ctt aaa gaa gaa				882
Arg Leu Ala Asp Gly Ser Leu Val Ala Val Lys Arg Leu Lys Glu Glu				
250		255		260
cga aca cca ggt ggt gag ctg cag ttt caa aca gag gtg gaa atg att				930
Arg Thr Pro Gly Gly Glu Leu Gln Phe Gln Thr Glu Val Glu Met Ile				
265		270		275
agc atg gct gtg cat cga aat ctt ctg cgt cta cgt ggt ttc tgc atg				978
Ser Met Ala Val His Arg Asn Leu Leu Arg Leu Arg Gly Phe Cys Met				
280		285		290
aca cca aca gag cgg ctt ctt gta tat cca tac atg gct aat gga agt				1026
Thr Pro Thr Glu Arg Leu Leu Val Tyr Pro Tyr Met Ala Asn Gly Ser				
300		305		310
gtt gcg tcg tgt tta aga gag cgt cag cca tca gaa cct ccc ctt gat				1074
Val Ala Ser Cys Leu Arg Glu Arg Gln Pro Ser Glu Pro Leu Asp				
315		320		325
tgg cca act agg aag agg att gca cta gga tct gct agg ggg ctt tct				1122
Trp Pro Thr Arg Lys Arg Ile Ala Leu Gly Ser Ala Arg Gly Leu Ser				
330		335		340
tat ttg cat gac cat tgt gat ccc aag att atc cat cgt gat gta aaa				1170
Tyr Leu His Asp His Cys Asp Pro Lys Ile Ile His Arg Asp Val Lys				
345		350		355

gct gca aat ata tta ttg gac gaa gaa ttt gag gct gtt gta ggt gat Ala Ala Asn Ile Leu Leu Asp Glu Glu Phe Glu Ala Val Val Gly Asp 360 365 370 375	1218
ttt ggg tta gct agg ctc atg gat tac aag gat acc cat gtt aca act Phe Gly Leu Ala Arg Leu Met Asp Tyr Lys Asp Thr His Val Thr Thr 380 385 390	1266
gct gta agg ggt acc ttg ggc tac ata gct ccc gag tac ctc tcg act Ala Val Arg Gly Thr Leu Gly Tyr Ile Ala Pro Glu Tyr Leu Ser Thr 395 400 405	1314
gga aag tca tca gag aag acc gat gtc ttt ggt tat ggg att atg ctc Gly Lys Ser Ser Glu Lys Thr Asp Val Phe Gly Tyr Gly Ile Met Leu 410 415 420	1362
tta gag ctc att act gga cag aga gct ttt gat ctt gct cgc ctt gcg Leu Glu Leu Ile Thr Gly Gln Arg Ala Phe Asp Leu Ala Arg Leu Ala 425 430 435	1410
aac gat gat gat gtt atg ttg ttg gat tgg gtt aaa agc ctt ttg aaa Asn Asp Asp Asp Val Met Leu Leu Asp Trp Val Lys Ser Leu Leu Lys 440 445 450 455	1458
gag aaa aag ttg gag atg ctg gtc gat cct gac ctg gag aac aat tac Glu Lys Lys Leu Glu Met Leu Val Asp Pro Asp Leu Glu Asn Asn Tyr 460 465 470	1506
att gac aca gaa gtt gag cag ctt att caa gta gca tta ctc tgt acc Ile Asp Thr Glu Val Glu Gln Leu Ile Gln Val Ala Leu Leu Cys Thr 475 480 485	1554
cag ggt tcg cca atg gag cg ^g cct aag atg tca gag gta gtc cga atg Gln Gly Ser Pro Met Glu Arg Pro Lys Met Ser Glu Val Val Arg Met 490 495 500	1602
ctt gaa ggt gat ggc ctt gca gaa aag tgg gac gag tgg caa aaa gta Leu Glu Gly Asp Gly Leu Ala Glu Lys Trp Asp Glu Trp Gln Lys Val 505 510 515	1650
gaa gtc atc cat caa gac gta gaa tta gct cca cat cga act tct gaa Glu Val Ile His Gln Asp Val Glu Leu Ala Pro His Arg Thr Ser Glu 520 525 530 535	1698
tgg atc cta gac tcg aca gat aac ttg cat gct ttt gaa tta tct ggt Trp Ile Leu Asp Ser Thr Asp Asn Leu His Ala Phe Glu Leu Ser Gly 540 545 550	1746
cca aga taaacagcat ataaaatgtg aatgaaatta atattttta tggtaaaaaa Pro Arg	1802
aaaaaaaaaaa aaa	1815
<210> 3	
<211> 553	

In re Application DeVries et al.
09/180,798

<212> PRT

<213> Daucus carota

<400> 3

Met Asn Arg Asn Ser Ile Asn Ile Leu Asn Tyr Met Gln Phe Thr Asp
1 5 10 15

Ala Tyr Leu Asp Lys Tyr Gly Val Leu Met Thr Leu Glu Leu Tyr Ser
20 25 30

Asn Asn Ile Ser Gly Pro Ile Pro Ser Asp Leu Gly Asn Leu Thr Asn
35 40 45

Leu Val Ser Leu Asp Leu Tyr Met Asn Ser Phe Ser Gly Pro Ile Pro
50 55 60

Asp Thr Leu Gly Lys Leu Thr Arg Leu Arg Phe Leu Arg Leu Asn Asn
65 70 75 80

Asn Ser Leu Ser Gly Pro Ile Pro Met Ser Leu Thr Asn Ile Thr Thr
85 90 95

Leu Gln Val Leu Asp Leu Ser Asn Asn Arg Leu Ser Gly Pro Val Pro
100 105 110

Asp Asn Gly Ser Phe Ser Leu Phe Thr Pro Ile Ser Phe Ala Asn Asn
115 120 125

Leu Asn Leu Cys Gly Pro Val Thr Gly Arg Pro Cys Pro Gly Ser Pro
130 135 140

Pro Phe Ser Pro Pro Pro Phe Ile Pro Pro Ser Thr Val Gln Pro
145 150 155 160

Pro Gly Gln Asn Gly Pro Thr Gly Ala Ile Ala Gly Gly Val Ala Ala
165 170 175

Gly Ala Ala Leu Leu Phe Ala Ala Pro Ala Met Ala Phe Ala Trp Trp
180 185 190

Arg Arg Arg Lys Pro Arg Glu His Phe Phe Asp Val Pro Ala Glu Glu
195 200 205

Asp Pro Glu Val His Leu Gly Gln Leu Lys Arg Phe Ser Leu Arg Glu
210 215 220

Leu Gln Val Ala Thr Asp Thr Phe Ser Thr Ile Leu Gly Arg Gly Gly
225 230 235 240

Phe Gly Lys Val Tyr Lys Gly Arg Leu Ala Asp Gly Ser Leu Val Ala
245 250 255

Val Lys Arg Leu Lys Glu Glu Arg Thr Pro Gly Gly Glu Leu Gln Phe
260 265 270

Gln Thr Glu Val Glu Met Ile Ser Met Ala Val His Arg Asn Leu Leu
275 280 285

09/180,798

Arg Leu Arg Gly Phe Cys Met Thr Pro Thr Glu Arg Leu Leu Val Tyr
 290 295 300
 Pro Tyr Met Ala Asn Gly Ser Val Ala Ser Cys Leu Arg Glu Arg Gln
 305 310 315 320
 Pro Ser Glu Pro Pro Leu Asp Trp Pro Thr Arg Lys Arg Ile Ala Leu
 325 330 335
 Gly Ser Ala Arg Gly Leu Ser Tyr Leu His Asp His Cys Asp Pro Lys
 340 345 350
 Ile Ile His Arg Asp Val Lys Ala Ala Asn Ile Leu Leu Asp Glu Glu
 355 360 365
 Phe Glu Ala Val Val Gly Asp Phe Gly Leu Ala Arg Leu Met Asp Tyr
 370 375 380
 Lys Asp Thr His Val Thr Thr Ala Val Arg Gly Thr Leu Gly Tyr Ile
 385 390 395 400
 Ala Pro Glu Tyr Leu Ser Thr Gly Lys Ser Ser Glu Lys Thr Asp Val
 405 410 415
 Phe Gly Tyr Gly Ile Met Leu Leu Glu Leu Ile Thr Gly Gln Arg Ala
 420 425 430
 Phe Asp Leu Ala Arg Leu Ala Asn Asp Asp Asp Val Met Leu Leu Asp
 435 440 445
 Trp Val Lys Ser Leu Leu Lys Glu Lys Lys Leu Glu Met Leu Val Asp
 450 455 460
 Pro Asp Leu Glu Asn Asn Tyr Ile Asp Thr Glu Val Glu Gln Leu Ile
 465 470 475 480
 Gln Val Ala Leu Leu Cys Thr Gln Gly Ser Pro Met Glu Arg Pro Lys
 485 490 495
 Met Ser Glu Val Val Arg Met Leu Glu Gly Asp Gly Leu Ala Glu Lys
 500 505 510
 Trp Asp Glu Trp Gln Lys Val Glu Val Ile His Gln Asp Val Glu Leu
 515 520 525
 Ala Pro His Arg Thr Ser Glu Trp Ile Leu Asp Ser Thr Asp Asn Leu
 530 535 540
 His Ala Phe Glu Leu Ser Gly Pro Arg
 545 550

<210> 4
 <211> 13
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 4

ttttttttt tgc

13

<210> 5

<211> 10

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 5

gggatctaag

10

<210> 6

<211> 10

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 6

acacgtggc

10

<210> 7

<211> 10

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 7

tcagcacagg

10

<210> 8

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 8

ttttttttt tctg

14

In re Application DeVries et al.
09/180,798

<210> 9
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 9
ttttttttt tca 13

<210> 10
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 10
gacatcggtcc 10

<210> 11
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 11
ccctactggc 10

<210> 12
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 12
acacgtggtc 10

<210> 13
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 13

ggtgactgtc

10

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 14

tcttggacca gataattc

18

<210> 15
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 15

ctctgatgac tttccagtc

19

<210> 16
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 16

aatggcattt gcatgg

16

<210> 17
<211> 5
<212> PRT
<213> Daucus carota

<400> 17

Ser Pro Pro Pro Pro
1 5

<210> 18
<211> 8
<212> PRT
<213> Daucus carota

<400> 18

His Arg Asp Val Lys Ala Ala Asn
1 5

<210> 19
<211> 9
<212> PRT
<213> Daucus carota

<400> 19
Gly Thr Leu Gly Tyr Ile Ala Pro Glu
1 5

<210> 20
<211> 4081
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> exon
<222> (1280)..(1366)

<400> 20
tctagaaacc ttttgatcat aatgaaaata aagagtccat ccaccacatg gggtaagcat 60
aatgtgtat atttaaaggg taacaaatgt aatctgcattt ttatttact ttttacctct 120
actcaaattt tatgggcagt tttttttttt ttttaaatga taagacaagt atctgtttaa 180
tggtatttgt atgaaacagt agtaaagtca tatcggcac gccatactac ttccacagtg 240
gaacttggcc aaattttgtc tttgccgtct ctacagtttcc ttccacccaaa ttttttgtt 300
acaaaaactca aatcttcaa ttcacatctctt gccaaagttt ggttagaaaa gaatatcagc 360
aaacactaat atctttatttgc ttgcatttttatg tatcaatcac aaaattcaca accattgtaa 420
aaaaaaaaatttcc acatttttgg tatgagattt ctcacatgtat agtgaacctc tttaacattt 480
taactttact ttccataataa cgggattacg aatcttactt gcattaaaaa ttttagaaaaag 540
gtttttctac tttaaaaaaa aagggaccca acagagagag gtttgaccag gagaaacggg 600
tgcatagcct taagagctt caactactttt accccaaacc caaagcgatg tcactttcaa 660
ccatcttttc tctcccccgaa acccgaaaaa ttgaccggcgtt agttcgccca gcagcaccgt 720
tacgggcagc ttatatttctt cgtttttctt ctctacacca ctgcattttccc ataaataaaag 780
cccggttggaa tctttaaaaa tattaaataa tatatcaacg aaaaagctat tttatttata 840
agaagaaaaa gagaggaaca acaacaacac actaatcata gtttctctgg caggcttgg 900
gttgcggctt aataaaaaagc tctttttttttt ttatttttttcc acgttagattt tccccaaaaa 960
gctttttttttt tttttttttttt aaaaaaaaaagt ttcatcttta ttcaactttt gttttacagt 1020
gtgtgtgtga gagagagagt gtgggttggat tgaggaaaga cgacgacgag aacgccccggag 1080

aattaggatt tttatTTTtat ttttactct ttgtttgttt taatgctaAT gggTTTTaa 1140
aagggttATC gaaaaaatga gtgagTTTgt gttgaggttg tctctgtaaa gtgttaatgg 1200
tggtgatTTT cggaagttAG ggttttctcg gatctgaaga gatcaaATca agattcgAAA 1260
tttagcattg ttgtttgaa atg gag tcg agt tat gtg gtg ttt atc tta ctt 1312
tca ctg atc tta ctt ccg aat cat tca ctg tgg ctt gct tct gct aat 1360
ttg gaa ggTCgtggT tactcaatta ctcagctta ctcgttCTC aattactttc 1416
tcgattctt tttatTTgga ggtgaatcgc tatcttagt gtctgcattt tgatttatga 1476
aaattgttGT tGtctttgt atttgtaaGA tttagTggct agtactttga atacactgtt 1536
ttgctttct tGtccagatc aactttgtat attgtAAagg catgttctt gggTTgaaaa 1596
gctgggttat ttgatATctt aagattgatg ttgttGatcc aaacattctc tGaaagactt 1656
catttGttt tggTTTgtA aagaatttgt ttaatttata gcctctaATc tcagagaggc 1716
ctgtttGAat agtctctct tGaaattAGa ctTTcacca attgatgcta attgtgtAGA 1776
tttGttGttc ttgttatAGG tgatgtttG catacttGA gggTTactct agttgatcca 1836
aacaatgtct tgcagAGctg ggatcctacG ctGtGAatc ctGcAcAtG gttccatgtc 1896
acttgcAaca acgagaACAG tGtcaTAAGA gtGtaAGct ttcttctact aatcccactt 1956
tttaaacttt gacctcagcg tggttaccga cattttgtt tctttgtca aatacagtGA 2016
tttgggaat gcagAGttat ctggccattt agttccAGAG ctGgtgtgc tcaagaattt 2076
gcagtatttG taagttccac ttatGcatca tGctttAACA aaacaatcc aagatttgac 2136
agaagaAGCA ctggagttac ctTTGtaat tGAAATctt ttaacaAGtt tcttattttc 2196
ttacagggag ctTTacAGta acaacataAC tggcccGatt cctAGtaatc ttggAAatct 2256
gacAAacttA gtGAGTTGG atcttactt aaacAGcttcc tccggtccta ttccggAAatc 2316
attgggaaAG ctTTcaaAGc tGAGATTct tGAGtatac atatGcttA cCGGctcAGt 2376
tacagtctt GttAatctt aggtttgtt ccaattttG actcttGct gaaaattttA 2436
catgcaAGAA tagccggctt aacaacaaca gtctcactgg gtcaattcct atgtcactGA 2496
ccaatattac tacccttcaa gtGttGtgag tccctctcatt aactttcatt tatgtctact 2556
tcattctccc tcagttgatt tGttGAGtta atgcacttAA ccttGatGGA tGcaACACAG 2616
agatctatca aataacAGAC tctctggttc agttccTGAC aatggctcct tctcactt 2676
cacacccatc aggttctatG atttaccttc ttGAGtttG tGtcaGtGtc 2736

In re Application DeVries et al.
09/180,798

tgaacttatt ctgaaacttt catttccttg tgcagtttg ctaataactt agacctatgt 2796
ggacctgtta caagtccaccc atgtcctgga tctccccgt tttctccctcc accacccttt 2856
attcaaccc ccccaagttc caccccgagt aagcctcctc ttttagttt acattatagg 2916
aaacagaaga tgaaatcttt gcttctctgt caatccttt tctcatataa ctcatcttgc 2976
caataaggca ataaccaaattt gatctaattt gatttcaggt gggtatggta taactggagc 3036
aatagctggt ggagttgctg caggtgctgc tttgctctt gctgctcctg caatagcctt 3096
tgcttggtgg cgacgaagaa agccactaga tattttcttc gatgtgcctg gtgagtttat 3156
tattegcatt agtttctgtt cttagccagc aattttgttt tgcagaaaag tatttggaaaca 3216
actgttaatg aaaatcaata cataagtcat tgttttttaa gttacaaact cttttgagta 3276
aaatctcgat tgcaaaatct ctatgcagcc gaagaagatc cagaagttca tctgggacag 3336
ctcaagaggt tttctttgcg ggagctacaa gtggcgagtg atgggttag taacaagaac 3396
atttgggca gaggtggggtt tggaaagtc tacaaggac gcttggcaga cggaactctt 3456
gttgcgtca agagactgaa ggaagagcga actccaggtg gagagctcca gtttcaaaca 3516
gaagtagaga tgataagtat ggcagttcat cgaaacctgt tgagattacg aggttctgt 3576
atgacaccga ccgagagatt gcttgtgtat ctttacatgg ccaatggaaag ttttgcctcg 3636
tgtctcagag gtaaaaaacta aacaattaaa catcttgc tctctctcaa ttactttgac 3696
gtgaagtgtt ttttcatgtt ttccctttag gtttcataat ttttggttac actaatgaca 3756
cagagaggcc accgtcacaa cctccgcttg attggccaac gcggaaagaga atcgcgcctag 3816
gctcagctcg aggtttgtct tacctacatg atcactgcga tccgaagatc attcaccgtg 3876
acgtaaaagc agcaaacatc ctcttagacg aagaattcga agcgggtgtt ggagatttcg 3936
ggttggcaaa gctaattggac tataaagaca ctcacgtgac aacagcagtc cgtggcacca 3996
tcggtcacat cgctccagaa tatctctcaa ccggaaaatc ttcagagaaa accgacgttt 4056
tcqgatacqg aatcatqctt ctaqa 4081

<210> 21
<211> 494
<212> PRT
<213> *Arabidopsis thaliana*

<400> 21
Met Glu Ser Ser Tyr Val Val Phe Ile Leu Leu Ser Leu Ile Leu Leu
1 5 10 15

In re Application DeVries et al.
09/180,798

Pro Asn His Ser Leu Trp Leu Ala Ser Ala Asn Leu Glu Gly Asp Ala
20 25 30

Leu His Thr Leu Arg Val Thr Leu Val Asp Pro Asn Asn Val Leu Gln
35 40 45

Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val Thr
50 55 60

Cys Asn Asn Glu Asn Ser Val Ile Arg Val Asp Leu Gly Asn Ala Glu
65 70 75 80

Leu Ser Gly His Leu Val Pro Glu Leu Gly Val Leu Lys Asn Leu Gln
85 90 95

Glu Leu Tyr Ser Asn Asn Ile Thr Gly Pro Ile Pro Ser Asn Leu Gly
100 105 110

Asn Leu Thr Asn Leu Val Ser Leu Asp Leu Tyr Leu Asn Ser Phe Ser
115 120 125

Gly Pro Ile Pro Glu Ser Leu Gly Lys Leu Ser Lys Leu Arg Phe Leu
130 135 140

Arg Leu Asn Asn Asn Ser Leu Thr Gly Ser Ile Pro Met Ser Leu Thr
145 150 155 160

Asn Ile Thr Thr Leu Gln Val Leu Asp Leu Ser Asn Asn Arg Leu Ser
165 170 175

Gly Ser Val Pro Asp Asn Gly Ser Phe Ser Leu Phe Thr Pro Ile Ser
180 185 190

Phe Ala Asn Asn Leu Asp Leu Cys Gly Pro Val Thr Ser His Pro Cys
195 200 205

Pro Gly Ser Pro Pro Phe Ser Pro Pro Pro Pro Phe Ile Gln Pro Pro
210 215 220

Pro Val Ser Thr Pro Ser Gly Tyr Gly Ile Thr Gly Ala Ile Ala Gly
225 230 235 240

Gly Val Ala Ala Gly Ala Ala Leu Leu Phe Ala Ala Pro Ala Ile Ala
245 250 255

Phe Ala Trp Trp Arg Arg Arg Lys Pro Leu Asp Ile Phe Phe Asp Val
260 265 270

Pro Ala Glu Glu Asp Pro Glu Val His Leu Gly Gln Leu Lys Arg Phe
275 280 285

Ser Leu Arg Glu Leu Gln Val Ala Ser Asp Gly Phe Ser Asn Lys Asn
290 295 300

Ile Leu Gly Arg Gly Gly Phe Gly Lys Val Tyr Lys Gly Arg Leu Ala
305 310 315 320

Asp Gly Thr Leu Val Ala Val Lys Arg Leu Lys Glu Glu Arg Thr Pro
325 330 335

Gly Gly Glu Leu Gln Phe Gln Thr Glu Val Glu Met Ile Ser Met Ala
340 345 350

Val His Arg Asn Leu Leu Arg Leu Arg Gly Phe Cys Met Thr Pro Thr
355 360 365

Glu Arg Leu Leu Val Tyr Pro Tyr Met Ala Asn Gly Ser Val Ala Ser
370 375 380

Cys Leu Arg Glu Arg Pro Pro Ser Gln Pro Pro Leu Asp Trp Pro Thr
385 390 395 400

Arg Lys Arg Ile Ala Leu Gly Ser Ala Arg Gly Leu Ser Tyr Leu His
405 410 415

Asp His Cys Asp Pro Lys Ile Ile His Arg Asp Val Lys Ala Ala Asn
420 425 430

Ile Leu Leu Asp Glu Glu Phe Glu Ala Val Val Gly Asp Phe Gly Leu
435 440 445

Ala Lys Leu Met Asp Tyr Lys Asp Thr His Val Thr Thr Ala Val Arg
450 455 460

Gly Thr Ile Gly His Ile Ala Pro Glu Tyr Leu Ser Thr Gly Lys Ser
465 470 475 480

Ser Glu Lys Thr Asp Val Phe Gly Tyr Gly Ile Met Leu Leu
485 490

<210> 22
<211> 1106
<212> DNA
<213> unknown

<220>
<221> CDS
<222> (142)..(795)

<400> 22
tcgaccacg cgtccgtcca acttcaataa aggggaaacc aacgtaaccc taatttgct 60
ttctcctctt tgttcagaaa atttccctt tactctcaa ttcctttcg attccctct 120
cttaaacctc cgaaagctca c atg gcg tct cga aac tat cgg tgg gag ctc 171
Met Ala Ser Arg Asn Tyr Arg Trp Glu Leu
1 5 10

ttc gca gct tcg tta acc cta acc tta gct ttg att cac ctg gtc gaa 219
Phe Ala Ala Ser Leu Thr Leu Thr Leu Ala Leu Ile His Leu Val Glu
15 20 25

gca aac tcc gaa gga gat gct ctc tac gct ctt cgc cgg agt ttg aca 267

Ala Asn Ser Glu Gly Asp Ala Leu Tyr Ala Leu Arg Arg Ser Leu Thr
30 35 40

gat cca gac cat gtc ctc cag agc tgg gat cca act ctt gtt aat cct 315
Asp Pro Asp His Val Leu Gln Ser Trp Asp Pro Thr Leu Val Asn Pro
45 50 55

tgt acc tgg ttc cat gtc acc tgt aac caa gac aac cgc gtc act cgt 363
Cys Thr Trp Phe His Val Thr Cys Asn Gln Asp Asn Arg Val Thr Arg
60 65 70

gtg gat ttg gga aat tca aac ctc tct gga cat ctt gcg cct gag ctt 411
Val Asp Leu Gly Asn Ser Asn Leu Ser Gly His Leu Ala Pro Glu Leu
75 80 85 90

ggg aag ctt gaa cat tta cag tat cta gag ctc tac aaa aac aac atc 459
Gly Lys Leu Glu His Leu Gln Tyr Leu Glu Leu Tyr Lys Asn Asn Ile
95 100 105

caa gga act ata cct tcc gaa ctt gga aat ctg aag aat ctc atc agc 507
Gln Gly Thr Ile Pro Ser Glu Leu Gly Asn Leu Lys Asn Leu Ile Ser
110 115 120

ttg gat ctg tac aac aac aat ctt aca ggg ata gtt ccc act ttc ttg 555
Leu Asp Leu Tyr Asn Asn Leu Thr Gly Ile Val Pro Thr Phe Leu
125 130 135

gga aaa ttg aag tct ctg gtc ttt tta cgg ctt aat gac aac cga ttg 603
Gly Lys Leu Lys Ser Leu Val Phe Leu Arg Leu Asn Asp Asn Arg Leu
140 145 150

acc ggt cca atc cta gag cac tca cgg caa tcc caa gcc ttt aaa gtt 651
Thr Gly Pro Ile Leu Glu His Ser Arg Gln Ser Gln Ala Phe Lys Val
155 160 165 170

gtt gac gtc tca agc aat gat ttg tgt ggg aca atc cca aca aac gga 699
Val Asp Val Ser Ser Asn Asp Leu Cys Gly Thr Ile Pro Thr Asn Gly
175 180 185

ccc ttt gct cac att cct tta cag aac ttt gag aac aac ccg aga ttg 747
Pro Phe Ala His Ile Pro Leu Gln Asn Phe Glu Asn Asn Pro Arg Leu
190 195 200

gag gga ccg gaa tta ctc ggt ctt gca agc tac gac act aac tgc acc 795
Glu Gly Pro Glu Leu Leu Gly Leu Ala Ser Tyr Asp Thr Asn Cys Thr
205 210 215

tgaaaacaact ggcaaaacct gaaaaatgaag aattgggggg tgaccttgta agaacacttc 855
accactttat caaatatcac atctattatg taataagtat atatatgttag taaaaacaaa 915
aaaaatgaag aatcgaatcg gtaatatcat ctggctcaa ttgagaactt cgaggctgt 975
atgtaaaatt tctaaatgcg attttcgctt actgtaatgt tcggttgtgg gattctgaga 1035
agtaacattt gtattggtat ggtatcaagt tggctgcct tggctgcata aaaaaaaaaa 1095

aaaaaaaaaa a

<210> 23
<211> 218
<212> PRT
<213> unknown

<400> 23
Met Ala Ser Arg Asn Tyr Arg Trp Glu Leu Phe Ala Ala Ser Leu Thr
1 5 10 15
Leu Thr Leu Ala Leu Ile His Leu Val Glu Ala Asn Ser Glu Gly Asp
20 25 30
Ala Leu Tyr Ala Leu Arg Arg Ser Leu Thr Asp Pro Asp His Val Leu
35 40 45
Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val
50 55 60
Thr Cys Asn Gln Asp Asn Arg Val Thr Arg Val Asp Leu Gly Asn Ser
65 70 75 80
Asn Leu Ser Gly His Leu Ala Pro Glu Leu Gly Lys Leu Glu His Leu
85 90 95
Gln Tyr Leu Glu Leu Tyr Lys Asn Asn Ile Gln Gly Thr Ile Pro Ser
100 105 110
Glu Leu Gly Asn Leu Lys Asn Leu Ile Ser Leu Asp Leu Tyr Asn Asn
115 120 125
Asn Leu Thr Gly Ile Val Pro Thr Phe Leu Gly Lys Leu Lys Ser Leu
130 135 140
Val Phe Leu Arg Leu Asn Asp Asn Arg Leu Thr Gly Pro Ile Leu Glu
145 150 155 160
His Ser Arg Gln Ser Gln Ala Phe Lys Val Val Asp Val Ser Ser Asn
165 170 175
Asp Leu Cys Gly Thr Ile Pro Thr Asn Gly Pro Phe Ala His Ile Pro
180 185 190
Leu Gln Asn Phe Glu Asn Asn Pro Arg Leu Glu Gly Pro Glu Leu Leu
195 200 205
Gly Leu Ala Ser Tyr Asp Thr Asn Cys Thr
210 215

<210> 24
<211> 981
<212> DNA
<213> unknown

<220>
<221> CDS
<222> (104)..(757)

<400> 24
agtgtgagta atttagtttgc ttcttcctc tttgttcaga aaattttccc ttactctca 60
aattcccttt cgattccct ctctaaacc tccgaaaagct cac atg gcg tct cga 115
Met Ala Ser Arg
1
aac tat cgg tgg gag ctc ttc gca gct tcg tta acc cta acc tta gct 163
Asn Tyr Arg Trp Glu Leu Phe Ala Ala Ser Leu Thr Leu Thr Leu Ala
5 10 15 20
ttg att cac ctg gtc gaa gca aac tcc gaa gga gat gct ctc tac gct 211
Leu Ile His Leu Val Glu Ala Asn Ser Glu Gly Asp Ala Leu Tyr Ala
25 30 35
ctt cgc cgg agt ttg aca gat cca gac cat gtc ctc cag agc tgg gat 259
Leu Arg Arg Ser Leu Thr Asp Pro Asp His Val Leu Gln Ser Trp Asp
40 45 50
cca act ctt gtt aat cct tgt acc tgg ttc cat gtc acc tgt aac caa 307
Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val Thr Cys Asn Gln
55 60 65
gac aac cgc gtc act cgt gtg gat ttg gga aat tca aac ctc tct gga 355
Asp Asn Arg Val Thr Arg Val Asp Leu Gly Asn Ser Asn Leu Ser Gly
70 75 80
cat ctt gcg cct gag ctt ggg aag ctt gaa cat tta cag tat cta gag 403
His Leu Ala Pro Glu Leu Gly Lys Leu Glu His Leu Gln Tyr Leu Glu
85 90 95 100
ctc tac aaa aac aac atc caa gga act ata cct tcc gaa ctt gga aat 451
Leu Tyr Lys Asn Asn Ile Gln Gly Thr Ile Pro Ser Glu Leu Gly Asn
105 110 115
ctg aag aat ctc atc agc ttg gat ctg tac aac aac aat ctt aca ggg 499
Leu Lys Asn Leu Ile Ser Leu Asp Leu Tyr Asn Asn Asn Leu Thr Gly
120 125 130
ata gtt ccc act tct ttg gga aaa ttg aag tct ctg gtc ttt tta cgg 547
Ile Val Pro Thr Ser Leu Gly Lys Leu Lys Ser Leu Val Phe Leu Arg
135 140 145
ctt aat gac aac cga ttg acc ggt cca atc cct aga gca ctc acg gca 595
Leu Asn Asp Asn Arg Leu Thr Gly Pro Ile Pro Arg Ala Leu Thr Ala
150 155 160
atc cca agc ctt aaa gtt gtc tca agc aat gat ttg tgt gga 643
Ile Pro Ser Leu Lys Val Val Asp Val Ser Ser Asn Asp Leu Cys Gly
165 170 175 180
aca atc cca aca aac gga ccc ttt gct cac att cct tta cag aac ttt 691

Thr Ile Pro Thr Asn Gly Pro Phe Ala His Ile Pro Leu Gln Asn Phe
185 190 195

gag aac aac ccg aga ttg gag gga ccg gaa tta ctc ggt ctt gca agc 739
Glu Asn Asn Pro Arg Leu Glu Gly Pro Glu Leu Leu Gly Leu Ala Ser
200 205 210

tac gac act aac tgc acc tgaaaacaact ggcaaaacct gaaaatgaag 787
Tyr Asp Thr Asn Cys Thr
215

aattgggggg tgaccttgta agaacacttc accacttat caaatatcac atctattatg 847
taataagtat atatatgttag taaaaacaaa aaaaatgaag aatcgaatcg gtaatatcat 907
ctggtctcaa ttgagaacct cgaggctgt atgtaaaatt tctaaatgctg attttcgcct 967
aaattactca cact 981

<210> 25
<211> 218
<212> PRT
<213> unknown

<400> 25
Met Ala Ser Arg Asn Tyr Arg Trp Glu Leu Phe Ala Ala Ser Leu Thr
1 5 10 15

Leu Thr Leu Ala Leu Ile His Leu Val Glu Ala Asn Ser Glu Gly Asp
20 25 30

Ala Leu Tyr Ala Leu Arg Arg Ser Leu Thr Asp Pro Asp His Val Leu
35 40 45

Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val
50 55 60

Thr Cys Asn Gln Asp Asn Arg Val Thr Arg Val Asp Leu Gly Asn Ser
65 70 75 80

Asn Leu Ser Gly His Leu Ala Pro Glu Leu Gly Lys Leu Glu His Leu
85 90 95

Gln Tyr Leu Glu Leu Tyr Lys Asn Asn Ile Gln Gly Thr Ile Pro Ser
100 105 110

Glu Leu Gly Asn Leu Lys Asn Leu Ile Ser Leu Asp Leu Tyr Asn Asn
115 120 125

Asn Leu Thr Gly Ile Val Pro Thr Ser Leu Gly Lys Leu Lys Ser Leu
130 135 140

Val Phe Leu Arg Leu Asn Asp Asn Arg Leu Thr Gly Pro Ile Pro Arg
145 150 155 160

Ala Leu Thr Ala Ile Pro Ser Leu Lys Val Val Asp Val Ser Ser Asn

165 170 175
Asp Leu Cys Gly Thr Ile Pro Thr Asn Gly Pro Phe Ala His Ile Pro
180 185 190

Leu Gln Asn Phe Glu Asn Asn Pro Arg Leu Glu Gly Pro Glu Leu Leu
195 200 205

Gly Leu Ala Ser Tyr Asp Thr Asn Cys Thr
210 215

<210> 26
<211> 789
<212> DNA
<213> unknown

<220>
<221> CDS
<222> (2)..(661)

<400> 26
t cga ccc acg cgt ccg cga aac tat cgg tgg gag ctc ttc gca gct tcg 49
Arg Pro Thr Arg Pro Arg Asn Tyr Arg Trp Glu Leu Phe Ala Ala Ser
1 5 10 15

tta atc cta acc tta gct ttg att cac ctg gtc gaa gca aac tcc gaa 97
Leu Ile Leu Thr Leu Ala Leu Ile His Leu Val Glu Ala Asn Ser Glu
20 25 30

gga gat gct ctt tac gct ctt cgc ccg agt tta aca gat ccg gac cat 145
Gly Asp Ala Leu Tyr Ala Leu Arg Arg Ser Leu Thr Asp Pro Asp His
35 40 45

gtt ctc cag agc tgg gat cca act ctt gtt aat cct tgt acc tgg ttc 193
Val Leu Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe
50 55 60

cat gtc acc tgt aac caa gac aac cgc gtc act cgt gtg gat ttg ggg 241
His Val Thr Cys Asn Gln Asp Asn Arg Val Thr Arg Val Asp Leu Gly
65 70 75 80

aat tca aac ctc tct gga cat ctt gcg cct gag ctt ggg aag ctt gaa 289
Asn Ser Asn Leu Ser Gly His Leu Ala Pro Glu Leu Gly Lys Leu Glu
85 90 95

cat tta cag tat cta gag ctc tac aaa aac aac atc caa gga act ata 337
His Leu Gln Tyr Leu Glu Leu Tyr Lys Asn Asn Ile Gln Gly Thr Ile
100 105 110

cct tcc gaa ctt gga aat ctg aag aat ctc atc agc ttg gat ctg tac 385
Pro Ser Glu Leu Gly Asn Leu Lys Asn Leu Ile Ser Leu Asp Leu Tyr
115 120 125

aac aac aat ctt aca ggg ata gtt ccc act tct ttg gga aaa ttg aag 433
Asn Asn Asn Leu Thr Gly Ile Val Pro Thr Ser Leu Gly Lys Leu Lys

130	135	140	
tct ctg gtc ttt tta cgg ctt aat gac aac cga ttg acg ggg cca atc Ser Leu Val Phe Leu Arg Leu Asn Asp Asn Arg Leu Thr Gly Pro Ile	481		
145	150	155	160
cct aga gca ctc act gca atc cca agc ctt aaa gtt gtt gat gtc tca Pro Arg Ala Leu Thr Ala Ile Pro Ser Leu Lys Val Val Asp Val Ser	529		
165	170	175	
agc aat gat ttg tgt gga aca atc cca aca aac gga cct ttt gct cac Ser Asn Asp Leu Cys Gly Thr Ile Pro Thr Asn Gly Pro Phe Ala His	577		
180	185	190	
att cct tta cag aac ttt gag aac aac ccg agg ttg gag gga ccg gaā Ile Pro Leu Gln Asn Phe Glu Asn Asn Pro Arg Leu Glu Gly Pro Glu	625		
195	200	205	
tta ctc ggt ctt gca agc tac gac act aac tgc acc tgaaaaaaatt Leu Leu Gly Leu Ala Ser Tyr Asp Thr Asn Cys Thr	671		
210	215	220	
ggcaaaacct gaaaatgaag aattgggggg tgaccttgta agaacacttc accactttat	731		
caaatatcac atctactatg taataagtat atatatgtag tccaaaaaaaa aaaaaaaaa	789		
<210> 27			
<211> 220			
<212> PRT			
<213> unknown			
<400> 27			
Arg Pro Thr Arg Pro Arg Asn Tyr Arg Trp Glu Leu Phe Ala Ala Ser			
1	5	10	15
Leu Ile Leu Thr Leu Ala Leu Ile His Leu Val Glu Ala Asn Ser Glu			
20	25	30	
Gly Asp Ala Leu Tyr Ala Leu Arg Arg Ser Leu Thr Asp Pro Asp His			
35	40	45	
Val Leu Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe			
50	55	60	
His Val Thr Cys Asn Gln Asp Asn Arg Val Thr Arg Val Asp Leu Gly			
65	70	75	80
Asn Ser Asn Leu Ser Gly His Leu Ala Pro Glu Leu Gly Lys Leu Glu			
85	90	95	
His Leu Gln Tyr Leu Glu Leu Tyr Lys Asn Asn Ile Gln Gly Thr Ile			
100	105	110	
Pro Ser Glu Leu Gly Asn Leu Lys Asn Leu Ile Ser Leu Asp Leu Tyr			
115	120	125	

Asn Asn Asn Leu Thr Gly Ile Val Pro Thr Ser Leu Gly Lys Leu Lys
130 135 140

Ser Leu Val Phe Leu Arg Leu Asn Asp Asn Arg Leu Thr Gly Pro Ile
145 150 155 160

Pro Arg Ala Leu Thr Ala Ile Pro Ser Leu Lys Val Val Asp Val Ser
165 170 175

Ser Asn Asp Leu Cys Gly Thr Ile Pro Thr Asn Gly Pro Phe Ala His
180 185 190

Ile Pro Leu Gln Asn Phe Glu Asn Asn Pro Arg Leu Glu Gly Pro Glu
195 200 205

Leu Leu Gly Leu Ala Ser Tyr Asp Thr Asn Cys Thr
210 215 220

<210> 28

<211> 894

<212> DNA

<213> unknown

<220>

<221> CDS

<222> (1)..(675)

<400> 28

gga ccg att caa gcc tcc gaa ggg gac gct ctt cac gcg ctt cgc cgg 48
Gly Pro Ile Gln Ala Ser Glu Gly Asp Ala Leu His Ala Leu Arg Arg
1 5 10 15

agc tta tca gat cca gac aat gtt gtt cag agt tgg gat cca act ctt 96
Ser Leu Ser Asp Pro Asp Asn Val Val Gln Ser Trp Asp Pro Thr Leu
20 25 30

gtt aat cct tgt act tgg ttt cat gtc act tgt aat caa cac cat caa 144
Val Asn Pro Cys Thr Trp Phe His Val Thr Cys Asn Gln His His Gln
35 40 45

gtc act cgt ctg gat ttg ggg aat tca aac tta tct gga cat cta gta 192
Val Thr Arg Leu Asp Leu Gly Asn Ser Asn Leu Ser Gly His Leu Val
50 55 60

cct gaa ctt ggg aag ctt gaa cat tta caa tat ctg tat gga atc atc 240
Pro Glu Leu Gly Lys Leu Glu His Leu Gln Tyr Leu Tyr Gly Ile Ile
65 70 75 80

act ctt ttg cct ttt gat tat ctg aaa aca ttt aca tta tca gtc aca 288
Thr Leu Leu Pro Phe Asp Tyr Leu Lys Thr Phe Thr Leu Ser Val Thr
85 90 95

cat ata aca ttt tgc ttt gag tca tat agt gaa ctc tac aaa aac gag 336
His Ile Thr Phe Cys Phe Glu Ser Tyr Ser Glu Leu Tyr Lys Asn Glu
100 105 110

att caa gga act ata cct tct gag ctt gga aat ctg aag agt cta atc 384
Ile Gln Gly Thr Ile Pro Ser Glu Leu Gly Asn Leu Lys Ser Leu Ile
115 120 125

agt ttg gat ctg tac aac aac aat ctc acc ggg aaa atc cca tct tct 432
Ser Leu Asp Leu Tyr Asn Asn Leu Thr Gly Lys Ile Pro Ser Ser
130 135 140

ttg gga aaa ttg aag tca ctt gtt ttt ttg cgg ctt aac gaa aac cga 480
Leu Gly Lys Leu Lys Ser Leu Val Phe Leu Arg Leu Asn Glu Asn Arg
145 150 155 160

ttg acc ggt cct att cct aga gaa ctc aca gtt att tca agc ctt aaa 528
Leu Thr Gly Pro Ile Pro Arg Glu Leu Thr Val Ile Ser Ser Leu Lys
165 170 175

gtt gtt gat gtc tca ggg aat gat ttg tgt gga aca att cca gta gaa 576
Val Val Asp Val Ser Gly Asn Asp Leu Cys Gly Thr Ile Pro Val Glu
180 185 190

gga cct ttt gaa cac att cct atg caa aac ttt gag aac aac ctg aga 624
Gly Pro Phe Glu His Ile Pro Met Gln Asn Phe Glu Asn Asn Leu Arg
195 200 205

ttg gag gga cca gaa cta cta ggt ctt gcg agc tat gac acc aat tgc 672
Leu Glu Gly Pro Glu Leu Leu Gly Leu Ala Ser Tyr Asp Thr Asn Cys
210 215 220

act taaaaagaag ttgaagaacc tataaagaag aatgttaggt gaccttgtaa 725
Thr
225

gaactctgta ccaagtgttt gttaaatctat atagaggcctt gttcatgtt atatatgaaa 785

gctttgagag acagtaactt gcaatgtatt ggtattggta gaaaaagttg aaatgagaat 845

tgctttgtaa ttggattgt gttcttatg taacttgaat ttcttatta 894

<210> 29
<211> 225
<212> PRT
<213> unknown

<400> 29
Gly Pro Ile Gln Ala Ser Glu Gly Asp Ala Leu His Ala Leu Arg Arg
1 5 10 15

Ser Leu Ser Asp Pro Asp Asn Val Val Gln Ser Trp Asp Pro Thr Leu
20 25 30

Val Asn Pro Cys Thr Trp Phe His Val Thr Cys Asn Gln His His Gln
35 40 45

Val Thr Arg Leu Asp Leu Gly Asn Ser Asn Leu Ser Gly His Leu Val
50 55 60

Pro Glu Leu Gly Lys Leu Glu His Leu Gln Tyr Leu Tyr Gly Ile Ile
65 70 75 80

Thr Leu Leu Pro Phe Asp Tyr Leu Lys Thr Phe Thr Leu Ser Val Thr
85 90 95

His Ile Thr Phe Cys Phe Glu Ser Tyr Ser Glu Leu Tyr Lys Asn Glu
100 105 110

Ile Gln Gly Thr Ile Pro Ser Glu Leu Gly Asn Leu Lys Ser Leu Ile
115 120 125

Ser Leu Asp Leu Tyr Asn Asn Leu Thr Gly Lys Ile Pro Ser Ser
130 135 140

Leu Gly Lys Leu Lys Ser Leu Val Phe Leu Arg Leu Asn Glu Asn Arg
145 150 155 160

Leu Thr Gly Pro Ile Pro Arg Glu Leu Thr Val Ile Ser Ser Leu Lys
165 170 175

Val Val Asp Val Ser Gly Asn Asp Leu Cys Gly Thr Ile Pro Val Glu
180 185 190

Gly Pro Phe Glu His Ile Pro Met Gln Asn Phe Glu Asn Asn Leu Arg
195 200 205

Leu Glu Gly Pro Glu Leu Leu Gly Leu Ala Ser Tyr Asp Thr Asn Cys
210 215 220

Thr
225

<210> 30
<211> 1063
<212> DNA
<213> unknown

<220>
<221> CDS
<222> (106)..(759)

<400> 30
tcgaccacg cgtccgacga aaccctaatt ttgcttcctc atcttgttca gaaaattact 60

caaattccta ttagattact ctctcttcga cctccgatag ctcac atg gcg tct cga 117
Met Ala Ser Arg
1

aac tat cgg tgg gag ctc ttc gca gct tcg tta atc cta acc tta gct 165
Asn Tyr Arg Trp Glu Leu Phe Ala Ala Ser Leu Ile Leu Thr Leu Ala
5 10 15 20

ttg att cac ctg gtc gaa gca aac tcc gaa gga gat gct ctt tac gct 213

Leu Ile His Leu Val Glu Ala Asn Ser Glu Gly Asp Ala Leu Tyr Ala
25 30 35

ctt cgc cggtt aca gat ccg gac cat gtt ctc cag agc tgg gat 261
Leu Arg Arg Ser Leu Thr Asp Pro Asp His Val Leu Gln Ser Trp Asp
40 45 50

cca act ctt gtt aat cct tgt acc tgg ttc cat gtc acc tgt aac caa 309
Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val Thr Cys Asn Gln
55 60 65

gac aac cgc gtc act cgt gtg gat ttg ggg aat tca aac ctc tct gga 357
Asp Asn Arg Val Thr Arg Val Asp Leu Gly Asn Ser Asn Leu Ser Gly
70 75 80

cat ctt gcg cct gag ctt ggg aag ctt gaa cat tta cag tat cta gag 405
His Leu Ala Pro Glu Leu Gly Lys Leu Glu His Leu Gln Tyr Leu Glu
85 90 95 100

ctc tac aaa aac aac atc caa gga act ata cct tcc gaa ctt gga aat 453
Leu Tyr Lys Asn Asn Ile Gln Gly Thr Ile Pro Ser Glu Leu Gly Asn
105 110 115

ctg aag aat ctc atc agc ttg gat ctg tac aac aac aat ctt aca ggg 501
Leu Lys Asn Leu Ile Ser Leu Asp Leu Tyr Asn Asn Leu Thr Gly
120 125 130

ata gtt ccc act tct ttg gga aaa ttg aag tct ctg gtc ttt tta cgg 549
Ile Val Pro Thr Ser Leu Gly Lys Leu Lys Ser Leu Val Phe Leu Arg
135 140 145

ctt aat gac aac cga ttg acg ggg cca atc cct aga gca ctc act gca 597
Leu Asn Asp Asn Arg Leu Thr Gly Pro Ile Pro Arg Ala Leu Thr Ala
150 155 160

atc cca agc ctt aaa gtt gtt gat gtc tca agc aat gat ttg tgt gga 645
Ile Pro Ser Leu Lys Val Val Asp Val Ser Ser Asn Asp Leu Cys Gly
165 170 175 180

aca atc cca aca aac gga cct ttt gct cac att cct tta cag aac ttt 693
Thr Ile Pro Thr Asn Gly Pro Phe Ala His Ile Pro Leu Gln Asn Phe
185 190 195

gag aac aac ccg agg ttg gag gga ccg gaa tta ctc ggt ctt gca agc 741
Glu Asn Asn Pro Arg Leu Glu Gly Pro Glu Leu Leu Gly Leu Ala Ser
200 205 210

tac gac act aac tgc acc tgaaaaatt ggcaaacct gaaaatgaag 789
Tyr Asp Thr Asn Cys Thr
215

aattgggggg tgaccttgta agaacacttc accactttat caaatatcac atctactatg 849

taataagtat atatatgttag tccaaaaaaaaaa aatgaagaa tcgaatcagt aatatcatct 909

ggctcaatt gagaactttg aggtctgtgt atgtaaaatt tctaaatgcg actttcgctg 969

actgtaatgt tcgggtgtgg gattctgaga agtaacattt gtattggat ggtatcaagt 1029
 1063
 tgttctgcct tgtctgcaaa aaaaaaaaaaaa aaaa

<210> 31
<211> 218
<212> PRT
<213> unknown

<400> 31
 Met Ala Ser Arg Asn Tyr Arg Trp Glu Leu Phe Ala Ala Ser Leu Ile 15
 1 5
 Leu Thr Leu Ala Leu Ile His Leu Val Glu Ala Asn Ser Glu Gly Asp 30
 20 25
 Ala Leu Tyr Ala Leu Arg Arg Ser Leu Thr Asp Pro Asp His Val Leu 45
 35 40
 Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val 60
 50 55
 Thr Cys Asn Gln Asp Asn Arg Val Thr Arg Val Asp Leu Gly Asn Ser 80
 65 70 75
 Asn Leu Ser Gly His Leu Ala Pro Glu Leu Gly Lys Leu Glu His Leu 95
 85 90
 Gln Tyr Leu Glu Leu Tyr Lys Asn Ile Gln Gly Thr Ile Pro Ser 110
 100 105
 Glu Leu Gly Asn Leu Lys Asn Leu Ile Ser Leu Asp Leu Tyr Asn Asn 125
 115 120
 Asn Leu Thr Gly Ile Val Pro Thr Ser Leu Gly Lys Leu Lys Ser Leu 140
 130 135
 Val Phe Leu Arg Leu Asn Asp Asn Arg Leu Thr Gly Pro Ile Pro Arg 160
 145 150 155
 Ala Leu Thr Ala Ile Pro Ser Leu Lys Val Val Asp Val Ser Ser Asn 175
 165 170
 Asp Leu Cys Gly Thr Ile Pro Thr Asn Gly Pro Phe Ala His Ile Pro 190
 180 185
 Leu Gln Asn Phe Glu Asn Asn Pro Arg Leu Glu Gly Pro Glu Leu Leu 205
 195 200
 Gly Leu Ala Ser Tyr Asp Thr Asn Cys Thr 215
 210

<210> 32
<211> 2089

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (195)..(2069)

<400> 32

ggattttat tttatttttt actctttgtt tgtttaatg ctaatgggtt tttaaaaggg 60
 ttatcgaaaa aatgagttagt gttgtgttga ggttgtctct gttaaagtgtt aatggtggtg 120
 attttcggaa gtttagggttt tctcggatct gaagagatca aatcaagatt cgaaatttac 180
 cattgttgtt tgaa atg gag tcg agt tat gtg gtg ttt atc tta ctt tca 230
 Met Glu Ser Ser Tyr Val Val Phe Ile Leu Leu Ser
 1 5 10

ctg atc tta ctt ccg aat cat tca ctg tgg ctt gct tct gct aat ttg 278
 Leu Ile Leu Leu Pro Asn His Ser Leu Trp Leu Ala Ser Ala Asn Leu
 15 20 25

gaa ggt gat gct ttg cat act ttg agg gtt act cta gtt gat cca aac 326
 Glu Gly Asp Ala Leu His Thr Leu Arg Val Thr Leu Val Asp Pro Asn
 30 35 40

aat gtc ttg cag agc tgg gat cct acg cta gtg aat cct tgc aca tgg 374
 Asn Val Leu Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp
 45 50 55 60

ttc cat gtc act tgc aac aac gag aac agt gtc ata aga gtt gat ttg 422
 Phe His Val Thr Cys Asn Asn Glu Asn Ser Val Ile Arg Val Asp Leu
 65 70 75

ggg aat gca gag tta tct ggc cat tta gtt cca gag ctt ggt gtg ctc 470
 Gly Asn Ala Glu Leu Ser Gly His Leu Val Pro Glu Leu Gly Val Leu
 80 85 90

aag aat ttg cag tat ttg gag ctt tac agt aac aac ata act ggc ccg 518
 Lys Asn Leu Gln Tyr Leu Glu Leu Tyr Ser Asn Asn Ile Thr Gly Pro
 95 100 105

att cct agt aat ctt gga aat ctg aca aac tta gtg agt ttg gat ctt 566
 Ile Pro Ser Asn Leu Gly Asn Leu Thr Asn Leu Val Ser Leu Asp Leu
 110 115 120

tac tta aac agc ttc tcc ggt cct att ccg gaa tca ttg gga aag ctt 614
 Tyr Leu Asn Ser Phe Ser Gly Pro Ile Pro Glu Ser Leu Gly Lys Leu
 125 130 135 140

tca aag ctg aga ttt ctc cgg ctt aac aac aac agt ctc act ggg tca 662
 Ser Lys Leu Arg Phe Leu Arg Leu Asn Asn Asn Ser Leu Thr Gly Ser
 145 150 155

att cct atg tca ctg acc aat att act acc ctt caa gtg tta gat cta 710
 Ile Pro Met Ser Leu Thr Asn Ile Thr Thr Leu Gln Val Leu Asp Leu
 160 165 170

tca aat aac aga ctc tct ggt tca gtt cct gac aat ggc tcc ttc tca Ser Asn Asn Arg Leu Ser Gly Ser Val Pro Asp Asn Gly Ser Phe Ser	758
175 180 185	
ctc ttc aca ccc atc agt ttt gct aat aac tta gac cta tgt gga cct Leu Phe Thr Pro Ile Ser Phe Ala Asn Asn Leu Asp Leu Cys Gly Pro	806
190 195 200	
gtt aca agt cac cca tgt cct gga tct ccc ccg ttt tct cct cca cca Val Thr Ser His Pro Cys Pro Gly Ser Pro Pro Phe Ser Pro Pro Pro	854
205 210 215 220	
cct ttt att caa cct ccc cca gtt tcc acc ccg agt ggg tat ggt ata Pro Phe Ile Gln Pro Pro Pro Val Ser Thr Pro Ser Gly Tyr Gly Ile	902
225 230 235	
act gga gca ata gct ggt gga gtt gct gca ggt gct gct ttg ccc ttt Thr Gly Ala Ile Ala Gly Gly Val Ala Ala Gly Ala Ala Leu Pro Phe	950
240 245 250	
gct gct cct gca ata gcc ttt gct tgg tgg cga cga aga agc cca cta Ala Ala Pro Ala Ile Ala Phe Ala Trp Trp Arg Arg Arg Ser Pro Leu	998
255 260 265	
gat att ttc ttc gat gtc cct gcc gaa gaa gat cca gaa gtt cat ctg Asp Ile Phe Phe Asp Val Pro Ala Glu Glu Asp Pro Glu Val His Leu	1046
270 275 280	
gga cag ctc aag agg ttt tct ttg cgg gag cta caa gtg gcg agt gat Gly Gln Leu Lys Arg Phe Ser Leu Arg Glu Leu Gln Val Ala Ser Asp	1094
285 290 295 300	
ggg ttt agt aac aag aac att ttg ggc aga ggt ggg ttt ggg aaa gtc Gly Phe Ser Asn Lys Asn Ile Leu Gly Arg Gly Phe Gly Lys Val	1142
305 310 315	
tac aag gga cgc ttg gca gac gga act ctt gtt gct gtc aag aga ctg Tyr Lys Gly Arg Leu Ala Asp Gly Thr Leu Val Ala Val Lys Arg Leu	1190
320 325 330	
aag gaa gag cga act cca ggt gga gag ctc cag ttt caa aca gaa gta Lys Glu Glu Arg Thr Pro Gly Gly Glu Leu Gln Phe Gln Thr Glu Val	1238
335 340 345	
gag atg ata agt atg gca gtt cat cga aac ctg ttg aga tta cga ggt Glu Met Ile Ser Met Ala Val His Arg Asn Leu Leu Arg Leu Arg Gly	1286
350 355 360	
ttc tgt atg aca ccg acc gag aga ttg ctt gtg tat cct tac atg gcc Phe Cys Met Thr Pro Thr Glu Arg Leu Leu Val Tyr Pro Tyr Met Ala	1334
365 370 375 380	
aat gga agt gtt gct tcg tgt ctc aga gag agg cca ccg tca caa cct Asn Gly Ser Val Ala Ser Cys Leu Arg Glu Arg Pro Pro Ser Gln Pro	1382
385 390 395	

ccg ctt gat tgg cca acg cg ^g aag aga atc gc ^g cta gg ^c tca gct cg ^a	1430		
Pro Leu Asp Trp Pro Thr Arg Lys Arg Ile Ala Leu Gly Ser Ala Arg			
400	405	410	
ggt ttg tct tac cta cat gat cac tgc gat ccg aag atc att cac cgt	1478		
Gly Leu Ser Tyr Leu His Asp His Cys Asp Pro Lys Ile Ile His Arg			
415	420	425	
gac gta aaa gca gca aac atc ctc tta gac gaa gaa ttc gaa gcg gtt	1526		
Asp Val Lys Ala Ala Asn Ile Leu Leu Asp Glu Glu Phe Glu Ala Val			
430	435	440	
gtt gga gat ttc ggg ttg gca aag ctt atg gac tat aaa gac act cac	1574		
Val Gly Asp Phe Gly Leu Ala Lys Leu Met Asp Tyr Lys Asp Thr His			
445	450	455	460
gtg aca aca gca gtc cgt ggc acc atc ggt cac atc gct cca gaa tat	1622		
Val Thr Thr Ala Val Arg Gly Thr Ile Gly His Ile Ala Pro Glu Tyr			
465	470	475	
ctc tca acc gga aaa tct tca gag aaa acc gac gtt ttc gga tac gga	1670		
Leu Ser Thr Gly Lys Ser Ser Glu Lys Thr Asp Val Phe Gly Tyr Gly			
480	485	490	
atc atg ctt cta gaa cta atc aca gga caa aga gct ttc gat ctc gct	1718		
Ile Met Leu Leu Glu Leu Ile Thr Gly Gln Arg Ala Phe Asp Leu Ala			
495	500	505	
cg ^g cta gct aac gac gac gtc atg tta ctt gac tgg gtg aaa gga	1766		
Arg Leu Ala Asn Asp Asp Asp Val Met Leu Leu Asp Trp Val Lys Gly			
510	515	520	
ttg ttg aag gag aag aag cta gag atg tta gtg gat cca gat ctt caa	1814		
Leu Leu Lys Glu Lys Lys Leu Glu Met Leu Val Asp Pro Asp Leu Gln			
525	530	535	540
aca aac tac gag gag aga gaa ctg gaa caa gtg ata caa gtg gcg ttg	1862		
Thr Asn Tyr Glu Glu Arg Glu Leu Glu Gln Val Ile Gln Val Ala Leu			
545	550	555	
cta tgc acg caa gga tca cca atg gaa aga cca aag atg tct gaa gtt	1910		
Leu Cys Thr Gln Gly Ser Pro Met Glu Arg Pro Lys Met Ser Glu Val			
560	565	570	
gta agg atg ctg gaa gga gat ggg ctt gc ^g gag aaa tgg gac gaa tgg	1958		
Val Arg Met Leu Glu Gly Asp Gly Leu Ala Glu Lys Trp Asp Glu Trp			
575	580	585	
caa aaa gtt gag att ttg agg gaa gag att gat ttg agt cct aat cct	2006		
Gln Lys Val Glu Ile Leu Arg Glu Glu Ile Asp Leu Ser Pro Asn Pro			
590	595	600	
aac tct gat tgg att ctt gat tct act tac aat ttg cac gcc gtt gag	2054		
Asn Ser Asp Trp Ile Leu Asp Ser Thr Tyr Asn Leu His Ala Val Glu			
605	610	615	620
tta tct ggt cca agg taaaaaaaaaaaaaaa aaaaaaaaaaaaaa	2089		

Leu Ser Gly Pro Arg
625

<210> 33
<211> 625
<212> PRT
<213> Arabidopsis thaliana

<400> 33 Met Glu Ser Ser Tyr Val Val Phe Ile Leu Leu Ser Leu Ile Leu Leu
1 5 10 15
Pro Asn His Ser Leu Trp Leu Ala Ser Ala Asn Leu Glu Gly Asp Ala
20 25 30
Leu His Thr Leu Arg Val Thr Leu Val Asp Pro Asn Asn Val Leu Gln
35 40 45
Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val Thr
50 55 60
Cys Asn Asn Glu Asn Ser Val Ile Arg Val Asp Leu Gly Asn Ala Glu
65 70 75 80
Leu Ser Gly His Leu Val Pro Glu Leu Gly Val Leu Lys Asn Leu Gln
85 90 95
Tyr Leu Glu Leu Tyr Ser Asn Asn Ile Thr Gly Pro Ile Pro Ser Asn
100 105 110
Leu Gly Asn Leu Thr Asn Leu Val Ser Leu Asp Leu Tyr Leu Asn Ser
115 120 125
Phe Ser Gly Pro Ile Pro Glu Ser Leu Gly Lys Leu Ser Lys Leu Arg
130 135 140
Phe Leu Arg Leu Asn Asn Asn Ser Leu Thr Gly Ser Ile Pro Met Ser
145 150 155 160
Leu Thr Asn Ile Thr Thr Leu Gln Val Leu Asp Leu Ser Asn Asn Arg
165 170 175
Leu Ser Gly Ser Val Pro Asp Asn Gly Ser Phe Ser Leu Phe Thr Pro
180 185 190
Ile Ser Phe Ala Asn Asn Leu Asp Leu Cys Gly Pro Val Thr Ser His
195 200 205
Pro Cys Pro Gly Ser Pro Pro Phe Ser Pro Pro Pro Phe Ile Gln
210 215 220
Pro Pro Pro Val Ser Thr Pro Ser Gly Tyr Gly Ile Thr Gly Ala Ile
225 230 235 240
Ala Gly Gly Val Ala Ala Gly Ala Ala Leu Pro Phe Ala Ala Pro Ala
245 250 255

Ile Ala Phe Ala Trp Trp Arg Arg Arg Ser Pro Leu Asp Ile Phe Phe
260 265 270

Asp Val Pro Ala Glu Glu Asp Pro Glu Val His Leu Gly Gln Leu Lys
275 280 285

Arg Phe Ser Leu Arg Glu Leu Gln Val Ala Ser Asp Gly Phe Ser Asn
290 295 300

Lys Asn Ile Leu Gly Arg Gly Gly Phe Gly Lys Val Tyr Lys Gly Arg
305 310 315 320

Leu Ala Asp Gly Thr Leu Val Ala Val Lys Arg Leu Lys Glu Glu Arg
325 330 335

Thr Pro Gly Gly Glu Leu Gln Phe Gln Thr Glu Val Glu Met Ile Ser
340 345 350

Met Ala Val His Arg Asn Leu Leu Arg Leu Arg Gly Phe Cys Met Thr
355 360 365

Pro Thr Glu Arg Leu Leu Val Tyr Pro Tyr Met Ala Asn Gly Ser Val
370 375 380

Ala Ser Cys Leu Arg Glu Arg Pro Pro Ser Gln Pro Pro Leu Asp Trp
385 390 395 400

Pro Thr Arg Lys Arg Ile Ala Leu Gly Ser Ala Arg Gly Leu Ser Tyr
405 410 415

Leu His Asp His Cys Asp Pro Lys Ile Ile His Arg Asp Val Lys Ala
420 425 430

Ala Asn Ile Leu Leu Asp Glu Glu Phe Glu Ala Val Val Gly Asp Phe
435 440 445

Gly Leu Ala Lys Leu Met Asp Tyr Lys Asp Thr His Val Thr Thr Ala
450 455 460

Val Arg Gly Thr Ile Gly His Ile Ala Pro Glu Tyr Leu Ser Thr Gly
465 470 475 480

Lys Ser Ser Glu Lys Thr Asp Val Phe Gly Tyr Gly Ile Met Leu Leu
485 490 495

Glu Leu Ile Thr Gly Gln Arg Ala Phe Asp Leu Ala Arg Leu Ala Asn
500 505 510

Asp Asp Asp Val Met Leu Leu Asp Trp Val Lys Gly Leu Leu Lys Glu
515 520 525

Lys Lys Leu Glu Met Leu Val Asp Pro Asp Leu Gln Thr Asn Tyr Glu
530 535 540

Glu Arg Glu Leu Glu Gln Val Ile Gln Val Ala Leu Leu Cys Thr Gln
545 550 555 560

In re Application DeVries et al.
09/180,798

Gly Ser Pro Met Glu Arg Pro Lys Met Ser Glu Val Val Arg Met Leu
565 570 575
Glu Gly Asp Gly Leu Ala Glu Lys Trp Asp Glu Trp Gln Lys Val Glu
580 585 590
Ile Leu Arg Glu Glu Ile Asp Leu Ser Pro Asn Pro Asn Ser Asp Trp
595 600 605
Ile Leu Asp Ser Thr Tyr Asn Leu His Ala Val Glu Leu Ser Gly Pro
610 615 620
Arg
625

33

1